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MDYGGALSAVGRELLFVTNPVVNGSVLVPEDQCYCAGWIE
SRGTNGAQTASNVLQWLAAGFSILLMFYAYQTWKSTCGWE
EIYVCAIEMVKVILEFFFEFKNPSMLYLATGHRVQWLRYAEWL
LTCPVILIHLSNLTGLSNDYSRRTMGLLVSDIGTIVWGATSAMA
TGYVKVIFFCLGLCYGANTFFHAAKAYIEGYHTVPGRCRQV
VTGMAWLFFVSWGMFPILFILGPEGFGVLSVYGSTVGHTIIDL
MSKNCWGLLGHYLRVLIHEHILIHGDIRKTTKLNIGGTEIEVETL
VEDEAEAGAVNKGTGKYASRESFLVMRDKMKEKGIDVRASL
DNSKEVEQEQAARAAMMMMNNGMGMGMGMNGMNGMG
GMNGMAGGAKPGLLELTPQLQPGRVILAVPDISMVDFFREQFA
QLSVTYELVPALGADNTLALVTQAQNLGGVDFVLIHPEFLRDR
SSTSILSRLRGAGQRVAAFGWAQLGPMRDLIESANLDGWLE
GPSFGQGILPAHIVALVAKMQQMRKMQQMQQIGMMTGGMN
GMGGGMGGGMNGMGGGNGMNNMGNGMGGGMGNGMG
NGMNGMGGGNGMNNMGNGMAGNGMGGGMGGNGMG
SMNGMSSGVVANVTPSAAGGMGGMMNGGMAAPQSPGMN
GGRLGTNPLFNAAPSPLSSQLGAEAGMGSMGGMGGMMSGM
GGMGGMGGMGGGAGAATTQAAGGNAEAEMLQNLNMNEINRL
KRELGE (SEQ ID NO:2)

Fig 1B

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MlptavegvsqAQITGRPEWIWLALGTALMGLGTLYFLVKGMGVS
DPDAKKFYAITTLVPAIAFTMYLSMLLGYGLTMVPFGGEQNPI
YWARYADWLFTTPLLLLDLALLVDADQGTLALVGADGIMIGT
GLVGALTKVYSYRFVWWAISTAAMLYILYVLFFGFTSKAESMR
PEVASTFKVLRNVTVVLWSAYPVWWLIGSEGAGIVPLNIETLLF
MVLDVSAKVGFGILLRSRAIFGEAEAPEPSAGDGAAATSD
(SEQ ID NO. 3)

Fig. 1C

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Chop1..MSRRPWLLALALAAGSAGASTGSDATVPVATQDGPDYVFHRAHERMI FQTSYTLEN 60
 Chop2.....MDYGGALS AVGREILFVTNPVV 23
 Bop.....M

* *
 Chop1..NGSVICIENNNGCECLAWLKN--GINAEKIAANILQWITFALSAICIMEYCYOHTKSTC 118
 Chop2..NGSVL-VPED-QCYCAGMIESR--GINGAQTASNVLOWLAAQFSIIL LMEIYAVQHTKSTC 79
 Bop..LPTAVEGVSQAQITGRPEWIIWLALGTALMG GTLYFLVKGMVSDPDACKK FYAI T TLVPA 51

* * * * *
 Chop1..GWERTYVATTEMIFIIYFHEHDEPAVI SSNGNKTVMERAEWILITCEVITIEHLSNIT 178
 Chop2..GWERTYCAITEMVIVLIEFFEEKNE SML LATCHRVQWERAEWILITCEVITIEHLSNIT 139
 Bop..IAFTMY---LSMLLGYGCLTMVPEGGEQ-----NPIYMAR DWTFTTPI LLD A-IL 100

* * * * *
 Chop1..GIANDYNKRTM-GLEVSDIGTIIVWGTIAALS KGVV-EVITFFLMGCHCIGIITFENAA-KVI 235
 Chop2..GLSNDYSRPTM-GLEVSDIGTIIVWCAISAMATGYV-KVITFFCLGICYGANIEFHAA-KAY 196
 Bop..V-DAT-Q-GTILA VGADGIMIGTGLVGAITIVSYEFVWVAISTAAAML ILYVLFFGFT 157

Fig. 1D

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Chop1... IEAYHHTVPKGCICRDLIRYLAMLYFCSWAMFFPVHILGPECFCHINQFNSAIAFAIIDIAS 295

Chop2... IEGYHHTVPKRCRQVVTGMWIFVSMGMPFIIFIIIGPECHALLSVYGSTVGTIIDIMS 256

Bop... SKAESMRPEV--ASTFKVIRNVTVVLMWSAYPVVWIIISECAGIVPLNIEITLLFMV D/SA 215

#

Chop1... KNATSMMGHELRVKIHEHHIILLYGDIPKKQKVIVAGQEMEVETMHEEDDETQKVP-TAK 354

Chop2... KNCWGLLGHYIRVLLIHEHII IHGDIRKTTKL IIGTETIEVEHILVEDEAEAGAVNKGTCKY 316

Bop... KVGEGLI--LIRSRAIFGEAEPEPSAGDGA-AATSD (Seq ID No. 3)

Chop1... ANRDSKIIMRRLKEKGFETRASLDGDPNGDAEANAAGGKPGMEMCKMTGMGMSMGAGM 414

Chop2... ASRESFLVMRDKMKEKCIDVRASLENSKEVEQQAARAAMMMNMGNGMGNGMNGMNGM 376

Chop1... GMATIDS-----GRVILAVPDISMVDFFEREQFARLPVPYELVPALGAENT 459

Chop2... GCMNGMAGGAKPGLLELTPQLQPGRVILAVPDISMVDFFEREQFAQLSVTYELVPALGADNT 436

Chop1... IQIVQQAQSLGGCDEVLMHPEFLPDRSPITGLIPRIKMGQRAAAFGWAALGEMRDLEGS 519

Chop2... IAIIVTQAQNLGGVDEVLIHPEFLPDRSSITISRLRGAGQVAAAFGWAQLGEMRDLESA 496

Chop1... GVDGWLLEGPSFCAGINQQALVALINRMQQAKRMGMG-----GMGMSMGCGMG-M 568

Chop2... NLDGWLLEGPSFCGCIIPAHIVALVAKMQQMRKMQQMQQIGMMTGGMNMGGMCGGMNGM 556

Fig. 1D (continued)

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Chop1... GCMCMG-MAPSMNAGMTGNGG-----ASMCG-----AVMSMCMGMQPMQQAMP--AMSPM 616
 Chop2... GGNGNNNGNGMGCGNGMNGMCGGNGMNNMGNMAGNMGGMGGNGMGGGS 616

Chop1... MTQQPS-MMSQPSAMSAGGAMQAMGGVMPSPAP-----GGRVCTNPLEFGSAPSPSSQ---- 667
 Chop2... MNGMSGGVVANVTPSAGGMGGMNNGMAAPQSPGMNGGRLGTNPLEFNAPSPSSQLGA 676

(Seq ID No. 1) Chop1... -----PGISPCMATPPAAATAAPAGGSEAEMEQQLMSFINPIN-ELGEEK 712
 (Seq ID No. 2) Chop2... EAGMGSMGGMGSMGGMGGMGGAGATTQAAGGNAEAEMEQNLMMELINPLKREIGH 737

Fig. 1D (continued)

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....5...10....5...20....5...30....5...40

MDYGGALSAVGRELLFVTNPVVVNGSVLVPEDQCYCAGWI	40
ESRGTNQAQTASNVLQWLAAGFSILLMFYAYQTWKSTCG	80
WEEIYVCAIEMVKVILEFFFFEFKNPSMLYLATGHRVQWLR	120
YAEWLLTCPVILIRLSNLTGLSNDYSRRTMGLLVSDIGTI	160
VWGATSAMATGYVKVIEFFCLGLCYGANTFFHAAKAYIEGY	200
HTVPKGRCRQVVTGMAWLFFVSWGMFPILFILGPEGFGVL	240
SVYGSTVGHTIIDLMSKNCWGLLGHYLRVLIHEHILIHGD	280
IRKTTKLNIGGTEIEVETLVEDEAEAGAVNKGTGK (SEQ ID NO. 4)	315

Fig. 1E